

EXHIBIT B: CLUSTAL W (1.7) MULTIPLE SEQUENCE ALIGNMENTS OF HUMAN MITOCHONDRIAL PROTEINS

Sequence format is Pearson

Sequence 1: HRM-19 (SEQ ID NO:19) 351 aa

Sequence 2: CGI-69 (AF151827_1) 351 aa

Sequence 3: CGI-69 L, mitochondrial carrier protein CGI-69 long form (AAG60687.1) 359 aa

Sequence 4: OGC, 2-oxoglutarate carrier protein (AAC28637.1) 314 aa

Pairwise alignments

Sequences (1:2) Aligned. Score: 99

Sequences (1:3) Aligned. Score: 99

Sequences (1:4) Aligned. Score: 21

Sequences (2:3) Aligned. Score: 99

Sequences (2:4) Aligned. Score: 21

Sequences (3:4) Aligned. Score: 19

CLUSTAL W (1.7) multiple sequence alignment

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HRM-19      MADQDPAGISPLQOMVASCTGAVVTSLFMTFLDVVKVRLQSQRPSMASELMPSSRLWSLS
CGI-69 L    MADQDPAGISPLQOMVASGTGAVVTSLFMTFLDVVKVRLQSQRPSMASELMPSSRLWSLS
CGI-69      MADQDPAGISPLQOMVASGTGAVVTSLFMTFLDVVKVRLQSQRPSMASELMPSSRLWSLS
OGC         -----MAATASAGAGGID-----G-----KP-RTS---PKSVKFLPG
              :  . : * : * : :  : *  : *  : *  : :
HRM-19      YTKW-----KCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHGCT
CGI-69 L    YTKLPSSLQSTGKCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHGCT
CGI-69      YTKW-----KCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHGCT
OGC         GLAG-----MGATVFVQPLDLVKNNRMQLSGEGAKTREYKTSFHALTSILKAEG
              :  . . : * * * * : :  . . . : * : * : * :
HRM-19      RTLWSGLPATLVMTVPATAIYFTAYDQLKAFLCGRALTS--DLYAPMVACALARLCTVTVI
CGI-69 L    RTLWSGLPATLVMTVPATAIYFTAYDQLKAFLCGRALTS--DIYAPMVAGALARLGTVTVI
CGI-69      RTLWSGLPATLVMTVPATAIYFTAYDQLKAFLCGRALTS--DLYAPMVAGALARJGTVTVI
OGC         RGIYTGLSAGLLRQATYTTTTLRLGIYTVLFERLTGADGTFPGFLLKAVICMTACATCAVVC
              * : * * * * * : : * * * * * : : * * * * * :
HRM-19      SPLELMRTKLQA-----QHVSYSR-ELGACVRTAVAQGGWRSWLWCWCPALRDVVFSA
CGI-69 L    SPLELMRTKLQA-----QHVSYSR-ELGACVRTAVAQGGWRSWLWCWCPALRDVVFSA
CGI-69      SPLELMRTKLQA-----QHVSYSR-ELGACVRTAVAQGGWRSWLWCWCPALRDVVFSA
OGC         TPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEG-VLTLLWRGCIPTMARAVVVNA
              : * * : : * : * : * : : * : * : * : * : * :
HRM-19      LYWFNYELVKSWNLNGLRPKDQTSVGMSFVAGGISGTVAAVLTLPFDVVKTQRQVALGAME
CGI-69 L    LYWFNYELVKSWNLNGLRPKDQTSVGMSFVAGGISGTVAAVLTLPFDVVKTQRQVALGAME
CGI-69      LYWFNYELVKSWNLNGLRPKDQTSVGMSFVAGGISGTVAAVLTLPFDVVKTQRQVALGAME
OGC         AQLASYSQSKQFLLDSGYFS-DNLLCHFCASMISGLVTTAASMPVDIAKTRIQN----MR
              . . . * : * : . : . * * * * * : : . . . * :
HRM-19      AVRVNPLHVDSTWLLLRIRAESETKGLFAGFLPRIIKAAPSCAIMISTYEFGKSFFQRL
CGI-69 L    AVRVNPLHVDSTWLLLRIRAESETKGLFAGFLPRIIKAAPSCAIMISTYEFGKSFFQRL
CGI-69      AVRVNPLHVDSTWLLLRIRAESETKGLFAGFLPRIIKAAPSCAIMISTYEFGKSFFQRL
OGC         MIDGKPEYKNGLDVLFKVRYE-GFFSLWKGFTPYYARLGPHTVLTFLFLEQMKNKAYKRL
              : : * : : . : * : * * * : * : * * : : * : : * :
HRM-19      NQDRLLGG
CGI-69 L    NQDRLLGG
CGI-69      NQDRLLGG
OGC         ----FLSG
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